

FIG. 1

| | | |
|-----|---|-----|
| 1 | CTCTAGATGTACATGGAGGATGACCGAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA | 60 |
| 1 | M T E K T N G V K S S P A N | 14 |
| 61 | TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC | 120 |
| 15 | N H N H H A P P A I K A N G K D D H R T | 34 |
| 121 | AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC | 180 |
| 35 | S S R P H S A A D D D T S S E L Q R L A | 54 |
| 181 | AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGGG | 240 |
| 55 | D V D A P Q Q G R S G F R R I V R L V G | 74 |
| 241 | GATCATCAGAGAATGGGCCAACAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT | 300 |
| 75 | I I R E W A N K N F R E E E P R P D S F | 94 |
| 301 | CCTCGAGCGTTTTCTGTGGGCCTGAACTCCAGACTGTGACCACACAGGAGGGGGATGGCAA | 360 |
| 95 | L E R F R G P E L Q T V T T Q E G D G K | 114 |
| 361 | AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA | 420 |
| 115 | G D K D G E D K G T K K K F E L F V L D | 134 |
| 421 | CCCAGCTGGGGATTTGTACTACTGCTGGCTATTTGTCTATTGCCATGCCCGTCCTTTACAA | 480 |
| 135 | P A G D L Y Y C W L F V I A M P V L Y N | 154 |
| 481 | CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT | 540 |
| 155 | W C L L V A R A C F S D L Q K G Y Y L V | 174 |
| 541 | GTGGCTGGTGTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT | 600 |
| 175 | W L V L D Y V S D V V Y I A D L F I R L | 194 |
| 601 | GCGCACAGGTTTCTGGAGCAGGGGCTGCTGGTCAAAGATACCAAGAACTGCGAGACAA | 660 |
| 195 | R T G F L E Q G L L V K D T K K L R D N | 214 |
| 661 | CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT | 720 |
| 215 | Y I H T L Q F K L D V A S I I P T D L I | 234 |
| 721 | CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCTGCTGCACTTTGC | 780 |
| 235 | Y F A V D I H S P E V R F N R L L H F A | 254 |
| 781 | CCGCATGTTTGAGTTCTTTGACCGACAGAGACACGCCAACTACCCTAACATCTTCCG | 840 |
| 255 | R M F E F F D R T E T R T N Y P N I F R | 274 |
| 841 | CATCAGCAACCTTGTCTCTACATCTTGGTCATCATCCACTGGAATGCCTGCATCTATTA | 900 |
| 275 | I S N L V L Y I L V I I H W N A C I Y Y | 294 |
| 901 | TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA | 960 |
| 295 | A I S K S I G F G V D T W V Y P N I T D | 314 |

FIG. 1 (Cont'd)

| | | |
|------|--|------|
| 961 | CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC | 1020 |
| 315 | P E Y G Y L A R E Y I Y C L Y W S T L T | 334 |
| 1021 | TCTCACTACCATTGGGGAGACACCACCCCTGTAAAGGATGAGGAGTACCTATTTGTCAT | 1080 |
| 335 | L T T I G E T P P P V K D E E Y L F V I | 354 |
| 1081 | CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT | 1140 |
| 355 | F D F L I G V L I F A T I V G N V G S M | 374 |
| 1141 | GATCTCCAACATGAATGCCACCCGGGCAGAGTTCAGGCTAAGATCGATGCCGTGAAACA | 1200 |
| 375 | I S N M N A T R A E F Q A K I D A V K H | 394 |
| 1201 | CTACATGCAGTTCCGAAAGGTCAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA | 1260 |
| 395 | Y M Q F R K V S K G M E A K V I R W F D | 414 |
| 1261 | CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC | 1320 |
| 415 | Y L W T N K K T V D E R E I L K N L P A | 434 |
| 1321 | CAAGCTCAGGGCTGAGATAGCCACCAATGTCCACTTGTCCACACTCAAGAAAGTGCGCAT | 1380 |
| 435 | K L R A E I A T N V H L S T L K K V R I | 454 |
| 1381 | CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT | 1440 |
| 455 | F H D C E A G L L V E L V L K L R P Q V | 474 |
| 1441 | CTTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT | 1500 |
| 475 | F S P G D Y I C R K G D I G K E M Y I I | 494 |
| 1501 | TAAGGAGGGCAAAGTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC | 1560 |
| 495 | K E G K L A V V A D D G V T Q Y A L L S | 514 |
| 1561 | GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA | 1620 |
| 515 | A G S C F G E I S I L N I K G S K M G N | 534 |
| 1621 | TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTCTTCTGCTGTGCAAGGA | 1680 |
| 535 | R R T A N I R S L G Y S D L F C L S K D | 554 |
| 1681 | TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCTTAGAAGAGAGGGG | 1740 |
| 555 | D L M E A V T E Y P D A K K V L E E R G | 574 |
| 1741 | TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA | 1800 |
| 575 | R E I L M K E G L L D E N E V A T S M E | 594 |
| 1801 | GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG | 1860 |
| 595 | V D V Q E K L G Q L E T N M E T L Y T R | 614 |
| 1861 | CTTTGGCCGCTGCTGGCTGAGTACCGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC | 1920 |
| 615 | F G R L L A E Y T G A Q Q K L K Q R I T | 634 |

FIG. 1 (Cont'd)

| | | |
|------|---|------|
| 1921 | AGTTCTGGAAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA | 1980 |
| 635 | V L E T K M K Q N N E D D Y L S D G M N | 654 |
| 1981 | CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG | 2040 |
| 655 | S P E L A A A D E P | 664 |
| 2041 | CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTACAT | 2100 |
| 2101 | GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGTCTCTGACCCTGNGTTTTTGGCC | 2160 |
| 2161 | TAAACATCCAAGATCCGCCTCGGAT | 2186 |

1921
635
1981
655
2041
2101
2161

FIG. 2

MTEKTNGVKSSPANNHNNHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAPQQGRSGFERRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGPQLTVTTQEGDGKGDGDGEDKGTKKKFELFVLDPAGD
LYYCWLFIAMPVLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIADLFIRLRTGFLEQGLLVKD
TKKLRDNYIHTLQFKLDVASIIPDLYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVVIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPPV
KDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNATRAEFQAKIDAVKHVMQFRKVS KGMEAKVIRWFD
YLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVRIFHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAAKVL EERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLLAE
YTGAQQKLKQRITVLETKMKQNNEDDYLS DGMNSPELAAADEP

FIG. 3

MTEKTNGVKSSPANNHNNHHAPPAIKANGKDDHRTSSRPHTSAADDDTSSELQRLADVDPQQGRSGFERRI
VRLVGIIREWANKNFREEEPDPDSFLERFRGPPELQTVTTQEGDGKGDGDGEDKGTKKKFELFVLD PAGD
LYYCWLFEVIAMPVLYNWCLLVARACFSDLQKGYLVWLVLVDYVSDVVYIADLFIRLRGTGFLEQGGLLVKD
TKKLRDNYIHTLQFKLDVASIIPDLDIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTTLTTIGETPPPV
KDEEYLFVIFDFLIGVLIFATIVGNVGSMSISNMNATRAEFQAKIDAVKHVMQFRKVS KGMEAKVIRWFD
YLWTKKTVDEREILKNLPAKLRAE IATNVHLSTLKKVRIFHDCEAGLLVELVLKLRPQV FSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKSGMGNRRRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAAKVL EERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRL LAE
YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

FIG. 4

| | | | | |
|------------|-------|--|---|-----|
| | | 1 | | 50 |
| HBYCNG | (1) | ----- | | |
| CNG2_BOS | (1) | ----- | | |
| CNG2_MOUSE | (1) | ----- | | |
| CNG2_RAT | (1) | ----- | | |
| rACNG | (1) | MSSWRSCARAPLSGSAWRRSAATRRSRCLKTKRKRWSSGKGTMPQSTQC | | |
| | | 51 | | 100 |
| HBYCNG | (1) | ----- | MTEKANGVKSSPANNHNNHAPPATIKANGKDDH | |
| CNG2_BOS | (1) | ----- | MTEKANGVKSSPANNHNNHAPPATIKASGKDDH | |
| CNG2_MOUSE | (1) | ----- | MMTEKSNGVKSSPANNHNNHPPPSIKANGKDDH | |
| CNG2_RAT | (1) | ----- | MMTEKSNGVKSSPANNHNNHPPPSIKANGKDDH | |
| rACNG | (51) | ETRRRAQTPCESTGHTWR | MMTEKSNGVKSSPANNHNNHPPATIKANGKDDH | |
| | | 101 | | 150 |
| HBYCNG | (33) | RTSSRPQ | SAADDDTSSSELQRLAEMDAPOQRGGFRRIARLVGVIREDWAN | |
| CNG2_BOS | (33) | RASSRPQ | SAADDDTSSSELQRLAEMDAPOQRGGFRRIARLVGVIREDWAN | |
| CNG2_MOUSE | (34) | RAGSRPQSV | AADDDTSSSELQRLAEMDAPOQRGGFRRIARLVGVIREDWAN | |
| CNG2_RAT | (34) | RAGSRPQSV | AADDDTSSSELQRLAEMDAPOQRGGFRRIARLVGVIREDWAN | |
| rACNG | (101) | RTSSRPQ | SAADDDTSSSELQRLAEMDAPOQRGGFRRIARLVGVIREDWAN | |
| | | 151 | | 200 |
| HBYCNG | (82) | KNFREEPRPDSFLERFRGPELOTVTTO | GDGKGDKDGEDGKTKKKFELE | |
| CNG2_BOS | (82) | KNFREEPRPDSFLERFRGPELOTVTTO | GDGKGDKDGEDGKTKKKFELE | |
| CNG2_MOUSE | (84) | KNFREEPRPDSFLERFRGPELOTVTTO | GDGKGDKDGEDGKTKKKFELE | |
| CNG2_RAT | (84) | KNFREEPRPDSFLERFRGPELOTVTTO | GDGKGDKDGEDGKTKKKFELE | |
| rACNG | (150) | KNFREEPRPDSFLERFRGPELOTVTTO | GDGKGDKDGEDGKTKKKFELE | |
| | | 201 | | 250 |
| HBYCNG | (132) | VLDPAGDL | YVWLVLDYV | |
| CNG2_BOS | (132) | VLDPAGDWYR | WLVLDYV | |
| CNG2_MOUSE | (134) | VLDPAGDWYR | WLVLDYV | |
| CNG2_RAT | (134) | VLDPAGDWYR | WLVLDYV | |
| rACNG | (200) | VLDPAGDWYR | WLVLDYV | |
| | | 251 | | 300 |
| HBYCNG | (182) | SDVVIADLFIRLRTGFLEQGLLVKD | TKKLRDNYIHTLQFKLDVASIIP | |
| CNG2_BOS | (182) | SDVVIADLFIRLRTGFLEQGLLVKD | TKKLRDNYIHTLQFKLDVASIIP | |
| CNG2_MOUSE | (184) | SDVVIADLFIRLRTGFLEQGLLVKD | PKKLRDNYIHTLQFKLDVASIIP | |
| CNG2_RAT | (184) | SDVVIADLFIRLRTGFLEQGLLVKD | PKKLRDNYIHTLQFKLDVASIIP | |
| rACNG | (250) | SDVVIADLFIRLRTGFLEQGLLVKD | PKKLRDNYIHTLQFKLDVASIIP | |
| | | 301 | | 350 |
| HBYCNG | (232) | DLIYFAVD | IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLY | |
| CNG2_BOS | (232) | DLIYFAVG | IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLY | |
| CNG2_MOUSE | (234) | DLIYFAVG | IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLY | |
| CNG2_RAT | (234) | DLIYFAVG | IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLY | |
| rACNG | (300) | DLIYFAVG | IHSPEVRFNRLHFARMFEFFDRTETRTSYPNIFRISNLVLY | |
| | | 351 | | 400 |
| HBYCNG | (282) | ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS | | |
| CNG2_BOS | (282) | ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS | | |
| CNG2_MOUSE | (284) | ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS | | |
| CNG2_RAT | (284) | ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS | | |
| rACNG | (350) | ILVLIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS | | |

FIG. 4 (Continued)

| | | | |
|------------|-------|---|-----|
| | | 401 | 450 |
| HBMYCNG | (332) | TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT | |
| CNG2_BOS | (332) | TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT | |
| CNG2_MOUSE | (334) | TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT | |
| CNG2_RAT | (334) | TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT | |
| rACNG | (400) | TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNAT | |
| | | 500 | |
| | | 451 | |
| HBMYCNG | (382) | RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN | |
| CNG2_BOS | (382) | RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN | |
| CNG2_MOUSE | (384) | RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN | |
| CNG2_RAT | (384) | RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN | |
| rACNG | (450) | RAEFQAKIDAVKHYMQFRKVSKEAKVIRWFDYLWTNKKTVDEREVLKN | |
| | | 550 | |
| | | 501 | |
| HBMYCNG | (432) | LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI | |
| CNG2_BOS | (432) | LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI | |
| CNG2_MOUSE | (434) | LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI | |
| CNG2_RAT | (434) | LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI | |
| rACNG | (500) | LPAKLRAEIAINVHLSTLKKVRIHQDCEAGLLVELVLKLRPQVFS PGDYI | |
| | | 600 | |
| | | 551 | |
| HBMYCNG | (482) | CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK | |
| CNG2_BOS | (482) | CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK | |
| CNG2_MOUSE | (484) | CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK | |
| CNG2_RAT | (484) | CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK | |
| rACNG | (550) | CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK | |
| | | 650 | |
| | | 601 | |
| HBMYCNG | (532) | MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE | |
| CNG2_BOS | (532) | MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE | |
| CNG2_MOUSE | (534) | MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE | |
| CNG2_RAT | (534) | MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE | |
| rACNG | (600) | MGNRRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAAKVLEERGREILMKE | |
| | | 700 | |
| | | 651 | |
| HBMYCNG | (582) | GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ | |
| CNG2_BOS | (582) | GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ | |
| CNG2_MOUSE | (584) | GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ | |
| CNG2_RAT | (584) | GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ | |
| rACNG | (650) | GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAAQOKLKQ | |
| | | 733 | |
| | | 701 | |
| HBMYCNG | (632) | RITVLETKMKONNEDDYLS DGMNSPELAAAEPP | |
| CNG2_BOS | (632) | RITVLETKMKONNEDDYLS DGMNSPEPPAEKP- | |
| CNG2_MOUSE | (634) | RITVLETKMKONNEDDYLS DGMNSPEPPAE-- | |
| CNG2_RAT | (634) | RITVLETKMKONNEDDYLS DGMNSPEPPAE-- | |
| rACNG | (700) | RITVLETKMKONNEDDYLS DGMNSPEPAAAEQP | |

FIG. 5

1 CTCTAGATGTACATGGAGGATGACCGAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA 60
 1 M T E K T N G V K S S P A N 14
 61 TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC 120
 15 N H N H H A P P A I K A N G K D D H R T 34
 121 AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC 180
 35 S S R P H S A A D D D T S S E L Q R L A 54
 181 AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGGG 240
 55 D V D A P Q Q G R S G F R R I V R L V G 74
 241 GATCATCAGAGAATGGGCCAACAAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT 300
 75 I I R E W A N K N F R E E E P R P D S F 94
 301 CCTCGAGCGTTTTTCGTGGGCTGAACTCCAGACTGTGACCACACAGGAGGGGATGGCAA 360
 95 L E R F R G P E L Q T V T T Q E G D G K 114
 361 AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA 420
 115 G D K D G E D K G T K K K F E L F V L D 134
 421 CCCAGCTGGGGATTTGTACTACTGCTGGCTATTGTGTCATTGCCATGCCCGTCTTTACAA 480
 135 P A G D L Y Y C W L F V I A M P V L Y N 154
 481 CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT 540
 155 W C L L V A R A C F S D L Q K G Y Y L V 174
 541 GTGGCTGGTGGTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT 600
 175 W L V L D Y V S D V V Y I A D L F I R L 194
 601 GCGCACAGGTTTCTGAGCAGGGGCTGCTGGTCAAAGATACCAAGAACTGCGAGACAA 660
 195 R T G F L E Q G L L V K D T K K L R D N 214
 661 CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT 720
 215 Y I H T L Q F K L D V A S I I P T D L I 234
 721 CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCTGCTGCACTTTGC 780
 235 Y F A V D I H S P E V R F N R L L H F A 254
 781 CCGCATGTTTGTAGTTCTTTGACCGACAGAGACACGCACCAACTACCCTAACATCTTCCG 840
 255 R M F E F F D R T E T R T N Y P N I F R 274
 841 CATCAGCAACCTTGTCTCTACATCTTGGTCATCATCCACTGGAATGCCCTGCATCTATTA 900
 275 I S N L V L Y I L V I I H W N A C I Y Y 294
 901 TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA 960
 295 A I S K S I G F G V D T W V Y P N I T D 314

FIG. 5 (Cont'd)

961 CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC 1020
 315 P E Y G Y L A R E Y I Y C L Y W S T L T 334

1021 TCTCACTACCATTGGGGAGACACCCCCCTGTAAAGGATGAGGAGTACCTATTGTGCAT 1080
 335 L T T I G E T P P P V K D E E Y L F V I 354

1081 CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT 1140
 355 F D F L I G V L I F A T I V G N V G S M 374

1141 GATCTCCAACATGAATGCCACCCGGGCAGAGTTCAGGCTAAGATCGATGCCGTGAAACA 1200
 375 I S N M N A T R A E F Q A K I D A V K H 394

1201 CTACATGCAGTTCCGAAAGGTGAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA 1260
 395 Y M Q F R K V S K G M E A K V I R W F D 414

1261 CTTACTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC 1320
 415 Y L W T N K K T V D E R E I L K N L P A 434

1321 CAAGCTCAGGGCTGAGATAGCCATCAATGTCCACTTGTCCACACTCAAGAAAGTGCGCAT 1380
 435 K L R A E I A I N V H L S T L K K V R I 454

1381 CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT 1440
 455 F H D C E A G L L V E L V L K L R P Q V 474

1441 CTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT 1500
 475 F S P G D Y I C R K G D I G K E M Y I I 494

1501 TAAGGAGGGCAAAGTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC 1560
 495 K E G K L A V V A D D G V T Q Y A L L S 514

1561 GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA 1620
 515 A G S C F G E I S I L N I K G S K M G N 534

1621 TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTTCTGCTTGTCCAAGGA 1680
 535 R R T A N I R S L G Y S D L F C L S K D 554

1681 TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCTTAGAAGAGAGGGG 1740
 555 D L M E A V T E Y P D A K K V L E E R G 574

1741 TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA 1800
 575 R E I L M K E G L L D E N E V A T S M E 594

1801 GGTGACGTCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG 1860
 595 V D V Q E K L G Q L E T N M E T L Y T R 614

1861 CTTTGGCCGCTGCTGGCTGAGTACACGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC 1920
 615 F G R L L A E Y T G A Q Q K L K Q R I T 634

FIG. 5 (Cont'd)

1921 AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGCCTCTCTGACCCTGGGTTTTTGCC 2160

2161 TAAACATCCAAGATTCCGCCTCGGATCCCG 2190

1921 AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA 1980
635 V L E T K M K Q N N E D D Y L S D G M N 654

1981 CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG 2040
655 S P E L A A A D E P 664

2041 CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTACAT 2100

2101 GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGCCTCTCTGACCCTGGGTTTTTGCC 2160

2161 TAAACATCCAAGATTCCGCCTCGGATCCCG 2190

FIG. 6

MTEKTNGVKSSPANNHNNHHAPPAIKANGKDDHRTSSRPHTSAADDDTSSELQRLADVDAPOQGRSGFRRI
VRLVGI IREWANKNFREEPRPDSFLERFRGPELQTVTTQEGDGKGDGEDKGTKKKFELFVLD PAGD
LYYCWL FVIAMPVLYNWCLLVARACFSDLQKGYLVWLVDYVSDVVIADLFIRLRGTGFLEQGGLLVKD
TKKLRDNYIHTLQFKLDVASI IPTDLIYFAVDIHSPEVRFNRLLHFARMFEFFDRTE TRTNYPNIFRIS
NLVLYILV IHHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTITGETPPP
KDEEYLFVIFDFLIGVLIFATIVGNVGS MISNMNATRAEFQAKIDAVKHYMQFRKVS KGMEAKVIRWFD
YLWTKKTVDEREILKNLP AKLRAEIAINVLSTLKKVRI FHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKSGKMGNNRTANIRSLGYSDLFCLS
KDDLMEAVTEYPD AAKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLAE
YTGAQQKLKQRITVLET KMKQNNEDDYLSDGMNSPELAADEP

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1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSSEL 50
  |||
1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSSEL 50

51 QRLADVDAPQQGRSGFRIRVRLVGIIREWANKNFREEEPRPDSFLERFRG 100
  |||
51 QRLADVDAPQQGRSGFRIRVRLVGIIREWANKNFREEEPRPDSFLERFRG 100

101 PELQTVTTQEGDGKGDKDGEDKGTKKKKFELFVLDPAGDLYYCWLFIAMP 150
  |||
101 PELQTVTTQEGDGKGDKDGEDKGTKKKKFELFVLDPAGDLYYCWLFIAMP 150

151 VLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIADLFIRLRTGFLE 200
  |||
151 VLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVIADLFIRLRTGFLE 200

201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250
  |||
201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250

251 LHFARMFEFFDRTETRTNPNIIFRISNLVLYILVLIHWNACIYYAISKSI 300
  |||
251 LHFARMFEFFDRTETRTNPNIIFRISNLVLYILVLIHWNACIYYAISKSI 300

301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEY 350
  |||
301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTIGETPPPVKDEEY 350

351 LFVIFDFLIGVLIFATIVGNVGSISMNATRAEFQAKIDAVKHYMQFRK 400
  |||
351 LFVIFDFLIGVLIFATIVGNVGSISMNATRAEFQAKIDAVKHYMQFRK 400

401 VSKGMEAKVIRWFDYLWTKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450
  |||
401 VSKGMEAKVIRWFDYLWTKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450

451 KVRIFHDCEAGLLVELVLKLRPQVFS PGDYICRKGDIGKEMYIIKEGKLA 500
  |||
451 KVRIFHDCEAGLLVELVLKLRPQVFS PGDYICRKGDIGKEMYIIKEGKLA 500

501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRRTANIRSLGYSDLFC 550
  |||
501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRRTANIRSLGYSDLFC 550

551 LSKDDLMEAVTEYPDAAKVLEERGRIILMKEGLLDENEVATSMEVDVQEK 600
  |||
551 LSKDDLMEAVTEYPDAAKVLEERGRIILMKEGLLDENEVATSMEVDVQEK 600

601 LGQLETNMETLYTRFGRLLAEYTGAQQKLRITVLETKMKQNNEDDYL 650
  |||
601 LGQLETNMETLYTRFGRLLAEYTGAQQKLRITVLETKMKQNNEDDYL 650

651 DGMNSPELAAADEP* 665
  |||
651 DGMNSPELAAADEP. 664

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